REMARKS

The above amendments to the above-captioned application along with the following remarks are being submitted as a full and complete response to the Official Action dated June 21, 2000, the period for response to which will expire on October 21, 2000.

In view of the above amendments and the following remarks, the Examiner is respectfully requested to give due reconsideration to this application, to indicate the allowability of the claims, and to pass this case to issue.

Claims 1-12 have been considered in this application. Claim 1 is being amended in order to more particularly define and distinctly claim applicants' invention. Claims 9, 10 and 12 are being cancelled without prejudice. Claim 13 is being added corresponding to other embodiments disclosed in the specification. Applicants hereby submit that no new matter is being introduced into the application through the submission of this response.

35 U.S.C. §112 Rejection

The examiner objects to claims 3-5 and 10 under the second paragraph of 35 U.S.C. § 112 because he does not know (1) what selection conditions "related" to GC content and/or Tm (claim 3), "further controls of third selecting means" (claim 5) and "which are collated each other" (claim 10) refer to; and (2) the support in the specification for "said prescribed base length"(claim 4) and "third selecting means"(claim5).

The description "a second selecting means" in page 21, line 13 of the specification was mistakenly stated as a third selecting means". Claim 3 has been amended to clarify that "said selection condition" determine the range of GC content and/or Tm of DNA nucleotides to be selected by a skilled in the art. Each specific value of GC content and TM varies depend on each nucleotide sequence of interest and the purpose of its use (page 20, line 16 to page 21, line 13).

As indicated, claim 10 has been cancelled and claims 3-5 has been amended in order to obviate the rejection. Accordingly, the withdrawal of the outstanding indefiniteness rejection under 35 U.S.C. §112 is in order, and is therefore respectfully solicited.

35 U.S.C. §101 Rejection

The examiner rejects to the subject matter of claims 9-10 under 35 U.S.C. § 101 due to the nonfunctional descriptive nature of the claimed storage medium. Rejections should be

obviated due to the cancellation of claims 9 and 10.

Prior Art Rejection

Claims 1-9 were rejected under 35 U.S.C. §102 as being anticipated by U.S. Pat. No. 5,176,995 to Sninski *et al.* (hereinafter "Sninski"). Claims 1, 4, 7-12 were rejected under 35 U.S.C. §102 as being anticipated by Kariko' article published on BioTechnigues (hereinafter "Kariko"). Claims 1-12 stand rejected under 35 U.S.C. § 103(a) as being unpatentable over Kariko in view of Sninski. The Examiner acknowledges that Kariko's lack of a second means for selecting DNA nucleotides, but Sninski is said to supply these teachings to avoid non-specific low yield PCR amplification of the gene of interest. Applicants respectfully traverse the rejection.

The present invention relates to a system for selecting certain partial sequences which meet predetermined conditions regarding base length, location, and the like based on the information of nucleotide sequences extracted from databases, as nucleotide sequences used for primers. Conventionally, primers were obtain by choosing a target sequence at first, then designing optimal sequences as primers against the target (page 3, lines 1-18). The present invention carriers out a series of operations, from inputting of nucleotide sequence information to determining sequences for primers with a single software (Fig. 5), which allow the design of a plurality of mutually different primers based on a plurality of mutually different DNA nucleotide sequence (lines 9-13, page 6.) information obtained from databases. In particular, the present invention excludes primers of the same chemical structure in lines 20-21, page 5 of the specification that "primers having differences in nucleotide sequences." In addition, the amendments positively recite predetermined genetic functions, such as cancer (line 16, page 5), which are used to screen DNA nucleotide sequences and to collate to the partial sequences, the primers, and hybridized DNA nucleotide sequences by their relevant positions on the original DNA nucleotide sequences (lines 9-13, page 6).

As a result, significant improvement of throughputs, such as amplification and analysis, are obtained by reducing redundant processing on the same primers. Via the invention, it becomes possible to design a plurality of all potential primers without choosing any one target DNA (Fig. 8; page 4 lines 21 to page 5) but a plurality of DNAs.

Independent claims 1, 7, 8 and 11 have been amended in order to clarify that a plurality of mutually different primer pairs are designed for a plurality of nucleotide sequence information according to the present invention. "A pair" refers to a pair of nucleotide sequences consisting of one located in 3« end and other located in 5« end for primers designed against one sequence of interest to be amplified (page 22, lines 19-26).

Applicants respectfully contend that there is no teaching of designing a plurality of mutually different primers based on mutually different DNA nucleotide sequence information

obtained from databases in Sninski or Kariko. In contrast, Sninski merely provides a method for detecting viruses by performing amplification and hybridization, and Kariko simply discloses a method for designing primers used for amplification of genes conserved among different species.

Secondly, neither of the references teaches or suggests one system automatically executing all analyzing steps via one software, form inputting of nucleotide sequence information, determining sequences for primers to collating the data of the premiers with the generic data of the DNA fragments amplified by PCR using the primers (page 27, line 20-22). Such an unique feature allows the present invention to record the position data of each partial sequences along the DNA nucleotide sequences. Then the invention collates the position information and the relevant genetic functions with the DNA sequences amplified from the primers.

Instead, Sninski discloses the method for determining nucleotide sequences suitable for amplification of target viruses either manually (col.5 line 68) or by using a combination of software, such as homology search programs. And Kariko discloses a method for determining sequences most suitable as PCR primers by performing well-known homology plot application, extracting partial consensus sequences, and using primer analysis software (page 1048, right column to page 1049, left column). It is significantly difficult to keep the information with several software packages regarding the positions and relevant genetic implication at each steps since different software are used at each step such that when more than 96 primers are used, it is impossible to store all the data in a medium.

As described above, both methods for designing primers are performed by combining different analysis software for determining conditions, such as homology. Although Kariko discloses determining sequences by using primer analysis software "Oligo Version 4.0", this software only displays information related to Tm or chemical structures such as pairing and loops of nucleotide sequences, but final determination is still made by a human based on such information. Sninski also describes Tm condition in selecting primers, but fails to describe any practical way to determine sequences (col. 10, line 35-64).

Accordingly, the withdrawal of the outstanding rejections under 35 U.S.C. §102(b) and § 103(a) is in order, and is respectfully solicited.

In view of all the above, clear and distinct differences as discussed exist between the present invention as now claimed and the prior art references upon which the rejections in the Office Action rely, Applicants respectfully contend that the prior art references cannot anticipate the present invention or render the present invention obvious. Rather, the present invention as a whole is distinguishable, and thereby allowable over the prior art.

Favorable reconsideration of this application as amended is respectfully solicited.

Should there be any outstanding issues requiring discussion that would further the prosecution and allowance of the above-captioned application, the Examiner is invited to contact the Applicants' undersigned representative at the address and phone number indicated below.

Respectfully submitted,

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